Alternatively, in one approach the oligonucleotides at the first quartile, the median and the third quartile of the cluster may be selected for experimental evaluation, indicated below by bold print.

GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAAAACTCATGTTCAAGA (target complement sequence) (SEQ ID NO: 9)

	T_m (°C)	ΔG_{MFOLD}	
~~GTCCAAAAAGGGTCAGTCTACCTCC~~	71.77	~~-1.20~~	SEQ ID NO: 10
~~TCCAAAAAGGGTCAGTCTACCTCCC~~	71.99	~~-1.20~~	SEQ ID NO: 11
~~CCAAAAAGGGTCAGTCTACCTCCCG~~	70.78	~~-1.20~~	SEQ ID NO: 12
~~CAAAAAGGGTCAGTCTACCTCCCGC~~	71.23	~~-1.20~~	SEQ ID NO: 13
~~AAAAAGGGTCAGTCTACCTCCCGCC~~	73.07	~~-1.20~~	SEQ ID NO: 14
~~AAAAGGGTCAGTCTACCTCCCGCCA~~	75.68	~~-1.20~~	SEQ ID NO: 15
~~AAAGGGTCAGTCTACCTCCCGCCAT~~	77.53	~~-1.20~~	SEQ ID NO: 16
~~AAGGGTCAGTCTACCTCCCGCCATA~~	79.03	~~-1.20~~	SEQ ID NO: 17
~~AGGGTCAGTCTACCTCCCGCCATAA~~	79.03	~~-1.20~~	SEQ ID NO: 18
~~GGGTCAGTCTACCTCCCGCCATAAA~~	76.85	~~-1.20~~	SEQ ID NO: 19
~~GGTCAGTCTACCTCCCGCCATAAAA~~	73.10	~~-0.80~~	SEQ ID NO: 20
GTCAGTCTACCTCCCGCCATAAAAA	69.50	0.90	SEQ ID NO: 21
TCAGTCTACCTCCCGCCATAAAAA	65.60	0.90	SEQ ID NO: 22
CAGTCTACCTCCCGCCATAAAAAAC	64.96	0.90	SEQ ID NO: 23
AGTCTACCTCCCGCCATAAAAAACT	65.48	1.10	SEQ ID NO: 24
GTCTACCTCCCGCCATAAAAAACTC	66.36	2.40	SEQ ID NO: 25
TCTACCTCCCGCCATAAAAAACTCA	64.97	2.90	SEQ ID NO: 26
CTACCTCCCGCCATAAAAAACTCAT	63.96	2.70	SEQ ID NO: 27
TACCTCCCGCCATAAAAAACTCATG	62.58	1.10	SEQ ID NO: 28
ACCTCCCGCCATAAAAAACTCATGT	65.10	0.40	SEQ ID NO: 29
CCTCCCGCCATAAAAAACTCATGTT	64.96	0.10	SEQ ID NO: 30
CTCCCGCCATAAAAAACTCATGTTC	63.37	-0.10	SEQ ID NO: 31
TCCCGCCATAAAAAACTCATGTTCA	62.86	-0.10	SEQ ID NO: 32
CCCGCCATAAAAAACTCATGTTCAA	60.47	-0.10	SEQ ID NO: 33
~~CCGCCATAAAAAACTCATGTTCAAG~~	~~57.98~~	-0.10	SEQ ID NO: 34
~~CGCCATAAAAAACTCATGTTCAAGA~~	~~56.20~~	-0.10	SEQ ID NO: 35

In the Claims

Please amend the claims as follows:

1. (**amended**) A method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence, said method comprising:

(a) identifying a predetermined number of unique oligonucleotides within a nucleotide sequence that is hybridizable with said target nucleotide sequence, said oligonucleotides being chosen to sample a length of said nucleotide sequence,

(b) determining and evaluating for each of said oligonucleotides at least one parameter that is predictive of the ability of each of said oligonucleotides to hybridize to said target nucleotide sequence,

(c) selecting a subset of oligonucleotides within said predetermined number of unique oligonucleotides based on an examination of said parameter,

(d) identifying oligonucleotides in said subset that are in clusters along a region of said nucleotide sequence that is hybridizable to said target nucleotide sequence and

(e) selecting, for a cluster, a hybridization oligonucleotide.

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98. **(amended)** A computer based method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence, said method comprising:

(a) identifying under computer control a predetermined number of unique oligonucleotides within a nucleotide sequence that is hybridizable with said target nucleotide sequence, said oligonucleotides being chosen to sample a length of said nucleotide sequence,

(b) under computer control, determining and evaluating for each of said oligonucleotides a value for at least one parameter that is predictive of the ability of each of said oligonucleotides to hybridize to said target nucleotide sequence and storing said parameter values,

(c) selecting under computer control, from said stored parameter values, a subset of oligonucleotides within said predetermined number of unique oligonucleotides based on an examination of said parameter,

(d) identifying under computer control oligonucleotides in said subset that are in clusters along a region of said nucleotide sequence that is hybridizable to said target nucleotide sequence and

(e) under computer control selecting, for a cluster, a hybridization oligonucleotide.

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100. **(amended)** A computer system for conducting a method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence, said method comprising:

(a) input means for introducing a target nucleotide sequence into said computer system,

(b) means for determining a number of unique oligonucleotides that are within a nucleotide sequence that is hybridizable with said target nucleotide sequence, said